



IFWO

RAW SEQUENCE LISTING

DATE: 08/16/2004

PATENT APPLICATION: US/10/698,808

TIME: 16:03:58

Input Set : N:\Crf4\Refhold\10_folder\J698808.raw

Output Set: N:\CRF4\08162004\J698808.raw

1 <110> APPLICANT: Adeokun, Anthonia Monisola
 2 Ambrose, Helen
 3 Cresswell, Carl
 4 Dudley, Adam
 5 <120> TITLE OF INVENTION: Chemical Compounds
 6 <130> FILE REFERENCE: 06275-264002
 7 <140> CURRENT APPLICATION NUMBER: US/10/698,808
 8 <141> CURRENT FILING DATE: 2003-10-03
 9 <150> PRIOR APPLICATION NUMBER: US 09/925,731
 10 <151> PRIOR FILING DATE: 2001-08-10
 11 <150> PRIOR APPLICATION NUMBER: US 60/226,909
 12 <151> PRIOR FILING DATE: 2000-08-23
 13 <160> NUMBER OF SEQ ID NOS: 12
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2452
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (100)...(2172)
 23 <400> SEQUENCE: 1
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 25 caacaacaaa aacatttgta tgatatctat atttcaatc atg gac caa aat caa 114
 26 Met Asp Gln Asn Gln
 27 1 5
 28 cat ttg aat aaa aca gca gag gca caa cct tca gag aat aag aaa aca 162
 29 His Leu Asn Lys Thr Ala Glu Ala Gln Pro Ser Glu Asn Lys Lys Thr
 30 10 15 20
 31 aga tac tgc aat gga ttg aag atg ttc ttg gca gct ctg tca ctc agc 210
 32 Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala Ala Leu Ser Leu Ser
 33 25 30 35
 34 ttt att gct aag aca cta ggt gca att att atg aaa agt tcc atc att 258
 35 Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met Lys Ser Ser Ile Ile
 36 40 45 50
 37 cat ata gaa cgg aga ttt gag ata tcc tct tct ctt gtt ggt ttt att 306
 38 His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser Leu Val Gly Phe Ile
 39 55 60 65
 40 gac gga agc ttt gaa att gga aat ttg ctt gtg att gta ttt gtg agt 354
 41 Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile Val Phe Val Ser
 42 70 75 80 85
 43 tac ttt gga tcc aaa cta cat aga cca aag tta att gga atc ggt tgt 402
 44 Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu Ile Gly Ile Gly Cys



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45		90		95		100		
46	ttc att atg gga att gga ggt gtt ttg act gct ttg cca cat ttc ttc						450	
47	Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala Leu Pro His Phe Phe							
48		105		110		115		
49	atg gga tat tac agg tat tct aaa gaa act aat atc aat tca tca gaa						498	
50	Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn Ile Asn Ser Ser Glu							
51		120		125		130		
52	aat tca aca tcg acc tta tcc act tgt tta att aat caa att tta tca						546	
53	Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile Asn Gln Ile Leu Ser							
54		135		140		145		
55	ctc aat aga gca tca cct gag ata gtg gga aaa ggt tgt tta aag gaa						594	
56	Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys Gly Cys Leu Lys Glu							
57		150		155		160		165
58	tct ggg tca tac atg tgg ata tat gtg ttc atg ggt aat atg ctt cgt						642	
59	Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met Gly Asn Met Leu Arg							
60		170		175		180		
61	gga ata ggg gag act ccc ata gta cca ctg ggg ctt tct tac att gat						690	
62	Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly Leu Ser Tyr Ile Asp							
63		185		190		195		
64	gat ttc gct aaa gaa gga cat tct tct ttg tat tta ggt ata ttg aat						738	
65	Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr Leu Gly Ile Leu Asn							
66		200		205		210		
67	gca ata gca atg att ggt cca atc att ggc ttt acc ctg gga tct ctg						786	
68	Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe Thr Leu Gly Ser Leu							
69		215		220		225		
70	ttt tct aaa atg tac gtg gat att gga tat gta gat cta agc act atc						834	
71	Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val Asp Leu Ser Thr Ile							
72		230		235		240		245
73	agg ata act cct act gat tct cga tgg gtt gga gct tgg tgg ctt aat						882	
74	Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly Ala Trp Trp Leu Asn							
75		250		255		260		
76	ttc ctt gtg tct gga cta ttc tcc att att tct tcc ata cca ttc ttt						930	
77	Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser Ser Ile Pro Phe Phe							
78		265		270		275		
79	ttc ttg ccc caa act cca aat aaa cca caa aaa gaa aga aaa gct tca						978	
80	Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys Glu Arg Lys Ala Ser							
81		280		285		290		
82	ctg tct ttg cat gtg ctg gaa aca aat gat gaa aag gat caa aca gct						1026	
83	Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu Lys Asp Gln Thr Ala							
84		295		300		305		
85	aat ttg acc aat caa gga aaa aat att acc aaa aat gtg act ggt ttt						1074	
86	Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys Asn Val Thr Gly Phe							
87		310		315		320		325
88	ttc cag tct ttt aaa agc atc ctt act aat ccc ctg tat gtt atg ttt						1122	
89	Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro Leu Tyr Val Met Phe							
90		330		335		340		
91	gtg ctt ttg acg ttg tta caa gta agc agc tat att ggt gct ttt act						1170	
92	Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr Ile Gly Ala Phe Thr							
93		345		350		355		

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94	tat gtc ttc aaa tac gta gag caa cag tat ggt cag cct tca tct aag	1218
95	Tyr Val Phe Lys Tyr Val Glu Gln Tyr Gly Gln Pro Ser Ser Lys	
96	360 365 370	
97	gct aac atc tta ttg gga gtc ata acc ata cct att ttt gca agt gga	1266
98	Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro Ile Phe Ala Ser Gly	
99	375 380 385	
100	atg ttt tta gga gga tat atc att aaa aaa ttc aaa ctg aac acc gtt	1314
101	Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe Lys Leu Asn Thr Val	
102	390 395 400 405	
103	gga att gcc aaa ttc tca tgt ttt act gct gtg atg tca ttg tcc ttt	1362
104	Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val Met Ser Leu Ser Phe	
105	410 415 420	
106	tac cta tta tat ttt ttc ata ctc tgt gaa aac aaa tca gtt gcc gga	1410
107	Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys Ser Val Ala Gly	
108	425 430 435	
109	cta acc atg acc tat gat gga aat aat cca gtg aca tct cat aga gat	1458
110	Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr Ser His Arg Asp	
111	440 445 450	
112	gta cca ctt tct tat tgc aac tca gac tgc aat tgt gat gaa agt caa	1506
113	Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys Asp Glu Ser Gln	
114	455 460 465	
115	tgg gaa cca gtc tgt gga aac aat gga ata act tac atc tca ccc tgt	1554
116	Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr Ile Ser Pro Cys	
117	470 475 480 485	
118	cta gca ggt tgc aaa tct tca agt ggc aat aaa aag cct ata gtg ttt	1602
119	Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys Lys Pro Ile Val Phe	
120	490 495 500	
121	tac aac tgc agt tgt ttg gaa gta act ggt ctc cag aac aga aat tac	1650
122	Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu Gln Asn Arg Asn Tyr	
123	505 510 515	
124	tca gcc cat ttg ggt gaa tgc cca aga gat gat gct tgt aca agg aaa	1698
125	Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp Ala Cys Thr Arg Lys	
126	520 525 530	
127	ttt tac ttt ttt gtt gca ata caa gtc ttg aat tta ttt ttc tct gca	1746
128	Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn Leu Phe Phe Ser Ala	
129	535 540 545	
130	ctt gga ggc acc tca cat gtc atg ctg att gtt aaa att gtt caa cct	1794
131	Leu Gly Gly Thr Ser His Val Met Leu Ile Val Lys Ile Val Gln Pro	
132	550 555 560 565	
133	gaa ttg aaa tca ctt gca ctg ggt ttc cac tca atg gtt ata cga gca	1842
134	Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser Met Val Ile Arg Ala	
135	570 575 580	
136	cta gga gga att cta gct cca ata tat ttt ggg gct ctg att gat aca	1890
137	Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly Ala Leu Ile Asp Thr	
138	585 590 595	
139	acg tgt ata aag tgg tcc acc aac aac tgt ggc aca cgt ggg tca tgt	1938
140	Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly Thr Arg Gly Ser Cys	
141	600 605 610	
142	agg aca tat aat tcc aca tca ttt tca agg gtc tac ttg ggc ttg tct	1986

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143 Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val Tyr Leu Gly Leu Ser
144      615                      620                      625
145 tca atg tta aga gtc tca tca ctt gtt tta tat att ata tta att tat      2034
146 Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr Ile Ile Leu Ile Tyr
147      630                      635                      640                      645
148 gcc atg aag aaa aaa tat caa gag aaa gat atc aat gca tca gaa aat      2082
149 Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile Asn Ala Ser Glu Asn
150                      650                      655                      660
151 gga agt gtc atg gat gaa gca aac tta gaa tcc tta aat aaa aat aaa      2130
152 Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser Leu Asn Lys Asn Lys
153                      665                      670                      675
154 cat ttt gtc cct tct gct ggg gca gat agt gaa aca cat tgt      2172
155 His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu Thr His Cys
156      680                      685                      690
157 taaggggaga aaaaaagcca cttctgcttc tgtgtttcca aacagcattg cattgattca      2232
158 gtaagatggt atttttgagg agttcctggt cctttcacta agaatttcca catcttttat      2292
159 ggtggaagta taaataagcc tatgaactta taataaaaca aactgtaggt agaaaaaatg      2352
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161 taaaattaa agtgagagac atggttactg tgtaataaaa      2452
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164 <211> LENGTH: 691
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 2
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169      1      5      10      15
170 Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
171      20      25      30
172 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
173      35      40      45
174 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
175      50      55      60
176 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
177      65      70      75      80
178 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
179      85      90      95
180 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
181      100      105      110
182 Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
183      115      120      125
184 Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
185      130      135      140
186 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
187      145      150      155      160
188 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
189      165      170      175
190 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
191      180      185      190
192 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr

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193																	
194	Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro	Ile	Ile	Gly	Phe	
195		210					215					220					
196	Thr	Leu	Gly	Ser	Leu	Phe	Ser	Lys	Met	Tyr	Val	Asp	Ile	Gly	Tyr	Val	
197		225				230					235					240	
198	Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser	Arg	Trp	Val	Gly	
199					245					250					255		
200	Ala	Trp	Trp	Leu	Asn	Phe	Leu	Val	Ser	Gly	Leu	Phe	Ser	Ile	Ile	Ser	
201				260				265						270			
202	Ser	Ile	Pro	Phe	Phe	Phe	Leu	Pro	Gln	Thr	Pro	Asn	Lys	Pro	Gln	Lys	
203			275					280					285				
204	Glu	Arg	Lys	Ala	Ser	Leu	Ser	Leu	His	Val	Leu	Glu	Thr	Asn	Asp	Glu	
205		290					295					300					
206	Lys	Asp	Gln	Thr	Ala	Asn	Leu	Thr	Asn	Gln	Gly	Lys	Asn	Ile	Thr	Lys	
207	305					310					315					320	
208	Asn	Val	Thr	Gly	Phe	Phe	Gln	Ser	Phe	Lys	Ser	Ile	Leu	Thr	Asn	Pro	
209					325					330					335		
210	Leu	Tyr	Val	Met	Phe	Val	Leu	Leu	Thr	Leu	Leu	Gln	Val	Ser	Ser	Tyr	
211				340					345					350			
212	Ile	Gly	Ala	Phe	Thr	Tyr	Val	Phe	Lys	Tyr	Val	Glu	Gln	Gln	Tyr	Gly	
213			355					360					365				
214	Gln	Pro	Ser	Ser	Lys	Ala	Asn	Ile	Leu	Leu	Gly	Val	Ile	Thr	Ile	Pro	
215		370					375					380					
216	Ile	Phe	Ala	Ser	Gly	Met	Phe	Leu	Gly	Gly	Tyr	Ile	Ile	Lys	Lys	Phe	
217	385					390					395					400	
218	Lys	Leu	Asn	Thr	Val	Gly	Ile	Ala	Lys	Phe	Ser	Cys	Phe	Thr	Ala	Val	
219					405					410					415		
220	Met	Ser	Leu	Ser	Phe	Tyr	Leu	Leu	Tyr	Phe	Phe	Ile	Leu	Cys	Glu	Asn	
221				420					425					430			
222	Lys	Ser	Val	Ala	Gly	Leu	Thr	Met	Thr	Tyr	Asp	Gly	Asn	Asn	Pro	Val	
223			435					440					445				
224	Thr	Ser	His	Arg	Asp	Val	Pro	Leu	Ser	Tyr	Cys	Asn	Ser	Asp	Cys	Asn	
225		450					455					460					
226	Cys	Asp	Glu	Ser	Gln	Trp	Glu	Pro	Val	Cys	Gly	Asn	Asn	Gly	Ile	Thr	
227	465					470					475					480	
228	Tyr	Ile	Ser	Pro	Cys	Leu	Ala	Gly	Cys	Lys	Ser	Ser	Ser	Gly	Asn	Lys	
229					485					490					495		
230	Lys	Pro	Ile	Val	Phe	Tyr	Asn	Cys	Ser	Cys	Leu	Glu	Val	Thr	Gly	Leu	
231				500					505					510			

VERIFICATION SUMMARY

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